

1/8

POLYMORPHISMS IN THE ICAM2 GENE

TGATTAATAT	TACCATTATT	GTAAACAATA	TTTGTTTGGA	GTTGTGTACT	
CATTTGCCAT	TTTATTTTCT	TGCCCTTCTT	TGCATAGCAA	ACTGTTCTGT	71100
AATCATTTTT	TCTTCTTACT	GAAGCACATT	TGTAAATGCT	CATTTAGGTA	
TTTTGGGGGA	TAAACTTTTT	GTTTATCTGT	TTTTGTTAAC	TTTGGTTCTT	71200
GAAAGATGGT	TTTGCTGGGT	ACACAATTCT	AATAGTTTTT	TTTTTTTTTC	
TTTCAAACAA	GAGAGGAAAG	TCACTGGATT	AGGACCCTGT	CAGAGCATAA	71300
TCCTTCCAAA	GCTCTGTGGG	AGAGATGAGT	TCACCTTCTA	AACTGAGACT	
CTAATCTCCC	CTCCCCCTCA	AAATTCTCTC	ACGTTTTCCA	GAACATCTT	71400
AACTCCTCCA	GTTTTATAGC	CCCCTTCCTT	GAGAAACTTA	GGGATCCAGA	
GAGCAAAACA	GGAGACATTT	CATGGTGAAA	ACAATTTTCC	AGGAAGGACC	71500
CCGAGTTTCT	TCTCTCTTCT	ACATCATGGT	CAGTTTCCTC	TTATTCCTGT	
GTTACAGGAC	CAACAGGTGT	GTAGGCCAC	TGCTGTGCAG	CAACAGGCCA	71600
ATTACACTGA	CACAGCAGGG	TTTCCTGCAG	AGAAAAAGTT	TAATGATCCC	
GGGGTGCCAA	ATGAGGAGAT	CGGGGAGACC	GTCAAATCCA	TCTCCCCAAA	71700
GAGTTCCTGGG	CTGGGATTTT	AGAGGACATT	GTGGAGGGCA	AGAGGCTGGT	
AAACTGGGGT	CAATGACTGG	TCGAGGTAAG	GGGATAAAAT	CACTGGAATA	71800
TGGAAACTGC	ATTCTTTTGT	GAGTCAGCTC	CTCTTGGGGT	CCTTCAGGCC	
AGCTGGCATC	AATTGGGTCC	TGCAGACTGG	CTGGCATCAG	TGGGGTCCTT	71900
CAGACCAGCC	TGCATGAGTA	CTTTCACTGG	TATGCAGGAC	CTGAAAGAAT	
ATCTCAAAGG	GAAAACTTAA	CATTTTATAA	TGTTCAAGCT	GTTACCTTTA	72000
GAGCAGTTAA	GGGAACTCTA	ATCCTATGAC	AGAGTCTGCA	TAATTCTGGG	
GCAATAGGCA	CCGAGCAACT	ATGAGGAAGC	AGGTCGAGAG	CATGCTGACC	72100
TAATGATTAA	TGTTGAGTGT	GCTGCAAGCT	CTTTTCCTGT	CGTGGACATT	
TTGTAGGGCA	AGCCCCACAG	TAACTCTCTG	TATGCAAGGT	GGTGGGCACC	72200
TGTAATCCTA	GCTACTCAGG	AGGCTGAGGC	AGGAGAATCA	CTTGAACCCA	
GGAGGCGGAC	GTTGCAGTGA	GCTGAGATTG	CATCACTGCA	CTCCAGCCTG	72300
GGTGACAGAG	CGAGACTCCA	TCTCAAAAAA	AGAAAACCTT	TGTGCAGGCC	
TAACCAAAG	TGCCCATCCT	CAAGGAGTAA	GGTACCATGA	TTGGCCTTGT	72400
TTACATTATA	AGGTCAGCCT	TGTGGACTTG	GGAAGCAGAG	ACTTTAGCAG	
TAGCAGGAGG	AAGATGCTGG	ACAAAAA	AAAAAACAGT	AAATGCTTAG	72500
GACCTAAAC	TAAAAACAGC	CTTCGCCCAG	GCTTGTTTAG	GACAAACTCT	
CTCATTCAAT	CACTAATCCA	TGCATGCACC	CATCCATCTA	CCAATTCAAC	72600
AATGATGAAG	CACCTACTGT	GTGCCAGGCA	GTGTCCTACA	CTGGGTGGAT	
GTAGCAGTAC	ATGAGATTCA	GCTTCTGCCC	TCACTGTTGA	TGGGCCAGTG	72700
GGGAGGCAGG	AAGGTTGATG	TGTCAACGGT	TAGAATACAG	TAACATTTTC	
TAACAAATAG	ATGGTCACAT	GCCCGGTGTG	TCCCAGCCAA	GCAGGGCCTG	72800
CCCAGGAAGG	ATGGGAGACA	TCACAGGAGG	AGATGGGGGG	TAGGAACTGG	
GGCCTGTGCT	TTCGGGGAGG	ACGTTGGGCT	GCAGAAGCCT	TGCTTGAAGA	72900
GGGAATCAGG	CTGGCCCTGC	TGTGTATGCA	GGTGGGATTC	CCAAGCACTG	
TCCCTTCCAG	AAGCTGTTTG	GAGCACTCCA	GGCATGGATC	ACCCACCTT	73000
CCCACAGTCC	CTCACAGTGA	GGCAGGCCCC	AGAACCTTCC	TCTGGCCTTC	
TGCTATGTTG	CTTTTCCCTC	TTGAGGGTCT	CCTGGGAACC	AGGCTCCTAA	73100
CAATCCTCTT	CTTGCGCCTG	CTCGGGCGGG	CTTCAACAGT	CACCATGGCA	
GGCTATCATT	CATGGTGACT	TCATTTTTTC	TAGGTATGTG	ATCTTGAACA	73200
AGTCATTTAA	CCTTGACGTG	CCTCAGTTTT	CCCATCTGTG	AGATGGAGAC	
AGTAACAGTA	CCTGCCTCAG	AGAGTTAGGG	GATTAATTGG	TTAATATTTA	73300
TAGAGTGCTT	GTGACAGTGC	CCGACTTGTA	GTAAGTAAAT	GTTTACTATT	
ATTATTATTG	ATGTTGTTAT	TGTTATTATT	ATTCTGACTC	AGTGGAGGAC	73400
ACAGAGTCTC	CACTACAGCA	ATGTCCCAT	CCCCACCCTT	CTGTCCCAGC	
CCCTGGCTTG	GGTTTCAGGA	GTGTTTCCTG	CTCTCAGGAC	TTTGCTGGCC	73500

FIGURE 1A

2/8

CCACATGAAA	TCAGATTCCT	TCAGGCTGGG	GGTGAAACTC	CACCCTGTTC	
TCCTTTTCTC	TGCTGGCCCC	AGGCCCTGCC	TCTTCCTCCC	TGCATCATT	73600
CCAAGTCCAG	CAACCCCGTC	CAGGGACTTC	CCTGGGTCCA	GGCTGACAAT	
GGCAGCCCTT	GATGGTTGTG	TACAGTAGTA	ACCGCCTTTG	CCCTCAGCAG	73700
TGAGGGAAGG	GCAGGACCTC	ACCCTGCCCT	CCCAACCCGG	AATGGAGCTT	
GGCCAAAGTC	CTGAGGATTC	TGGGGCATCC	CTTTGGAAAG	GCCCCATCAG	73800
GGGTTCCCTT	GAGAAAGCAA	GAAGTCCTGC	TCTTTCCCTG	CCTGGTTGCA	
AAAGGGATCT	TAGGCAGAAC	TGAGGGATGA	GACTGTGTGG	CGATCCCCCA	73900
GGAAGGTCCT	CTCGTCCATT	GAAATCCCTC	CCTTACCTGC	TCACTGCTTC	
TGCGGATTCC	TCCCTAGGAA	TAAAGTGAAA	CACCTCAGGC	TCCAACCCTC	74000
CCAACCCAAG	GCTCCCTCCT	GGAGGGAGAG	AGAGGATGGA	GGACATCAGG	
TAGGCCAGGA	AATGAAGGCC	ATGGTTTGGG	GGTGTGGCTG	CAGCCAGACT	74100
GACCCCATTC	TCTGTCTGTG	CCTGGGTTCG	TGGGGACTAT	TATGGGATGC	
ATTTCCTGAG	GCTCTGGGCC	TCAAGTTGGC	CCTGAATCAG	CTGAGTCAAG	74200
ATCAAGTCTA	GGTTGAAAAC	TGAGTGAGGG	CCAGGTGCGG	TGGCTCAGGC	
CTGTAATCCC	AGCACTTTGG	GAGGCCAAGG	CAGGCAGATC	ACCTGAGGTC	74300
AGGAGTTCAA	GACCAGCCTA	GACAACATGG	TGAAACCCCA	TCTCTATTAA	
AAATACAAAA	TTAGCTGGGT	GTGGTGACGC	GATCCTGTAA	TGTCAGCTAC	74400
TCTGGAGGCT	GAGGCAGGAG	AATTGCTTGA	ATCTGGGAGG	CAGAGGTTGC	
AGTGAACCAA	AAATTGTGCC	ACAGCACTCC	AGCCTGGGCG	ACAAGAGTGA	74500
GACTCCATCT	CAAAAAAAAA	AAGAAAAAGA	AAAAGAAAAG	AAAAGTGAAGT	
GGGATGTGAA	GGTTTATGCA	GAATTGCACC	AGGCATTTAG	CAGGAGAAGC	74600
TCAAATTGCC	CTCCAGGCTT	CCTTAGAAAA	GCCCAAGTCA	CTGTCCCCTT	
TTGCTATGGT	AACTGCAAGT	CCTGGACAGG	TCCTGGCCTT	TGGATGCTTG	74700
			G		
TCTCCCAGGC	ATGACTCCAA	CAATGCATCC	CATGGGATTT	GGGGTTCCCC	
AGATCTGGGG	CTTGTAGGCC	TGACTCTCCC	CTGTGCACAC	GTCTCATACA	74800
CGCATGCGTG	CACCCATTGC	CTGCCCCGCC	CCTTGACACAG	GGAGTCAGCA	
GGGAGGACTG	GGTTATGCCC	TGCTTATCAG	CAGCTTCCCA	GCTTCCTCTG	74900
CCTGGATTCT	TAGAGGCCTG	GGGTCCTAGA	ACGAGCTGGT	GCACGTGGCT	
TCCCAAAGAT	CTCTCAGATA	ATGAGAGGAA	ATGCAGTCAT	CAGTTTGCAG	75000
AAGGCTAGGG	ATTCTGGGCC	ATAGCTCAGA	CCTGCGCCCA	CCATCTCCCT	
CCAGGCAGCC	CTTGGCTGGT	CCCTGCGAGC	CCGTGGAGAC	TGCCAGAGAT	75100
	[exon 1: 75099..				
GTCCTCTTTC	GGTTACAGGA	CCCTGACTGT	GGCCCTCTTC	ACCCTGATCT	
	T		G		
GCTGTCCAGG	TAAGCCAGTT	TCCTGGGGTT	CCTGATTTGG	CACATGCCAG	75200
	..75159]				
CCGAGAGGGT	GGGGGTGCCC	TGTTCCCTGT	GGCTTCAGGT	GGAAGAGAAG	
	C				
TCCCAAAGT	TGCTGAGGTT	CTTAGGTTTT	TTTGTTTTGT	TTTAAGACAG	75300
GGTCTCGGTC	TATCACCCAG	GCTGGAGTAC	AGTGGCATGA	TCATGGCTCA	
CTGCACCTCC	CTGGGCTCGG	GTGATCCTCC	CACCTCAGCC	TCCTGAGTAG	75400
CTGGGATCAC	AGGTGAGAGC	CACCATGCCC	AGCTAATTTT	TGTATTTTTT	
GTAGAGATGG	CAGGGGCTGG	TCTCGAACTC	CTGGACTCAA	GTGATCCACC	75500
CGCCTTGGTC	TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	CACCATGCCC	
AGCCTGCTGA	AGCTTTTTAA	ATTTTTTATT	TTTATTATAG	GCAGGTTTCT	75600
GTTCTGTTGC	CCAGGCTGGA	GTGCAGGGTG	TGATCATAGC	TCACTGCAGC	
CTCCAACTCC	TGGGCTCAAC	AATCCTCCTG	CCCCAGCCTT	TGCACTGCTG	75700
GCCCCCTTCC	CCTGGATCAC	TGCCCCCAAG	TATCTGCAGG	GCGTGCCACG	
CCCCTGCATG	CCTTTGCCCA	CAGAGTCACC	ATCTGGGTGA	GGCCTTCATT	75800
GAGCACAGTA	TTTAAAGTGG	CCTCACCCCC	ACTCCCTGCT	CCCTTTCTCG	

FIGURE 1B

3/8

GCGCTTTCCT GCCATCTGAC CGCTGGGTGC TCTGCCTGTC ACTGTTTACT 75900
 GGAGCTCCGC CAGGGCAGTG TTTGGTCTAC TGTGATCACT GCTGTATCCC
 CAGAGCCTGA TGCTTTGGAC ATAGCAGGTG TTCAAAAAGT GTTTGTGCAA 76000
 GAAAGGAAGG GAGGGAGGGC TACAGAGGGC CCTCTGTGGG AGGGCTTTAT
 GGGGGAGGGG ACATTTGGGC TGACCTTAAA GACTGAGTCG GATCCCACTC 76100
 CATGGAGTTG GAGCACAGCC TGAGGAAGAC TAATCTGGAG CTGATGGGCA
 GATGGGCTGG AGGAAGGAGA GGCAGAGGCA GGGTGTGAGC TAGGGGGCTG 76200
 GAGGAAGGAC AGCCAGAGGC AGGGAGCCAG CTGGGGGGTG GCCTCCTGGT
 CTAGCCGGGG CCATGACACC TGACAAGGGG AAAGTAGCAG CGGGGTCCCC 76300
 AATGACCTTT CCTCTTCAGT CCCTGACCCA GGAGCCAGAC TGCCCTCAATG
 G
 GACAGCTCCA CTGGAGGGCA GGGGGTGGGG GGATGACACG ACTGCCCAGT 76400
 GTTTCTGGTT TTCCAGGATC GGATGAGAAG GTATTGAGG TACACGTGAG
 [exon 2: 76417..
 GCCAAAGAAG CTGGCGGTTG AGCCCAAAGG GTCCCTCGAG GTCAACTGCA 76500
 GCACCACCTG TAACCAGCCT GAAGTGGGTG GTCTGGAGAC CTCTCTAGAT
 AAGATTCTGC TGGACGAACA GGCTCAGTGG AAACATTACT TGGTCTCAAA 76600
 CATCTCCCAT GACACGGTCC TCCAATGCCA CTTACCTGC TCCGGGAAGC
 AGGAGTCAAT GAATTCCAAC GTCAGCGTGT ACCGTGAGTG GCTGTGCTGC 76700
 ..76683]
 GGGGCCCTCC TCTCCCCTGG GACAGAGGCT GTGTCTACTG AATGCACACA
 GAGCCCCTCT GTGCCTGCTC CTGGGCACTG TCATCGTGGG GCCCTGCCTC 76800
 CCTGAGCTCC TGGGGTGACA AGGGGCAGGA CCAGGCCAGC CCTTGGTTGG
 ATGCCTTGAG CCCGCTGGCA TCTCAAGACG CAGACAACCC ACATTTTGAG 76900
 TCTTGCTTAG GGGAGGACAA TCTAACCAAC ATTTAGCCAA ATCCAGAAGT
 CATTTCCCAA CATAGCTGAG TCACCAGAGC ACCCATGTC CCATGCCAAG 77000
 TAGTGGGGTC ACCATCAGGG GAGCTGAGCC TGTCCATCTC ATGGCAAGAA
 GGTTGAAGTG TCGCCCAGGG TTTTATCTT CCCCTCAGGG CCCACAGCAA 77100
 ATGTGTGGCC ATCACACTCC ACCTGCACAT GAGCCATGAA AACCTTCCAG
 ATGGGCTGGG ATAGGACATC TTGGCGCTAA GGGTATCACC TGGGTCCATT 77200
 CCATCACCAG TTTCAGTGGA TCAATGAACA GAAAAACATC TTAAATCCAA
 CATATTTTCT CGGGGTGGGA GGTGGGGTGA GTGGAAGTGA AGTATTCTAA 77300
 TTCAAAAGAG AATCCAGGGC ACCCCTCGG GTGGTTGAAT ACGTGAGGAA
 TCGTGGTGGC CATGGCCCTG ACCCTGGAGA ACCTGGGCAG GTCTGGCTCT 77400
 GGCTCTGCC TCCTAAGTGA TGAACCTCAC AGCTCAGTTC CTCCAGTGCC
 CAGTTCAGT GAGCAATGCC CATCTAAGTC TCTCTCAACG TGATCACCCA 77500
 ACTGTTTAAT GTTTGAAATT TATATTTTCT TTCTGAAGGA GAGGAGACAG
 ACCCAAACCT TTATATCTTT CCAGTTGGCT GTACAATTTT TGAACCTTGT 77600
 CCTTGTAGAC ACCTGGTCAC CGGAAACCAT CATGTCTGTA AAATACTACC 77700
 ACAGTCCAGC CTCCATCCTC AACTGCTGCC CTCTTCTCT CTGCACTGGA
 GCCGGCCAGG CCACCTCCTC CCCAACCCTG GAACACCATG GTGACAGGAG
 ATGGCCCTGG CCAGGGGGAG GCTGCTGGGA CTGCACCCCC ATCCTGACCA 77800
 GACCTCCCTC CTTTGTCCCC TGCAGAGCCT CCAAGGCAGG TCATCCTGAC
 [exon 3: 77826..
 ACTGCAACCC ACTTTGGTGG CTGTGGGCAA GTCCTTCACC ATTGAGTGCA 77900
 GGGTGCCAC CGTGGAGCCC CTGGACAGCC TCACCCTCTT CCTGTTCCGT
 GGCAATGAGA CTCTGCACTA TGAGACCTTC GGGAAGGCAG CCCCTGCTCC 78000
 GCAGGAGGCC ACAGCCACAT TCAACAGCAC GGCTGACAGA GAGGATGGCC
 ACCGCAACTT CTCCTGCCTG GCTGTGCTGG ACTTGATGTC TCGCGGTGGC 78100
 AACATCTTTC ACAAACACTC AGCCCCGAAG ATGTTGGAGA TCTATGGTGA
 ..78145]

FIGURE 1C

4/8

GGGGGGATCC	GTGGATGGAG	TTGGGAGTGA	TAAGTCACTT	TCAGCCCCTC	78200
A			G G		
GGGGGAAGAA	AAATCTTGAG	TCCCACTTGG	GAAGCAAACA	CCCAGGAGCC	
CACCCTTCAT	CCTGAGGCTT	CCCTCTTACT	CTCCCTCTTC	CCTGAAGTTC	78300
TTTCCAAGTC	CCCAGCTTGG	ACCTCAACTG	CTCCAGAGGT	CGGGAGAGGT	
CAACTAGTTC	CTCGGCCACC	ATCAAGCCCC	ATGACCTTGA	CGGCTCTCCC	78400
TGGCCTTGGC	TCCCCTCCAC	AATGAGAAGT	TTGGCCTGAC	TGCCCCCACT	
GAGGTCCCCA	GAGCTCTGCT	GCTTGGTGAC	CCTGGACGGC	CGGCACACAG	78500
GGAGCCTGGC	ATGAAGTTCA	CTCAGCTCTG	CCCAAGAAGG	GGCTTGGCTG	
GGACCATGCC	ACCCTCCAGG	CCACGGTGTC	CAGCAGCTAC	ACACTGGTCC	78600
CATGGCTGCT	GACAAGGGGA	CATCTGCCCT	CACAGCCACA	CAGAAGTCCA	
GCTGGTAGCC	TGAGCCCTGG	GCCACCTTTT	TTCCAGATAA	TAATTTTAAT	78700
GCAGACACCA	TTCAECCACTC	ATCTCTGCAA	CTGGGGTGAC	TGCTGGATGC	
ATGAGCGGGC	GGCGGGGTCT	GGGGGTCTGG	GTTGGGGGTG	GACTTCCACT	78800
CCCTTTTGGT	CCCTGGTAAC	TGGGATCACA	GGACGTCTAA	GACCCTTGCC	
CCCTCCCTCC	CCAGAGCCTG	TGTCGGACAG	CCAGATGGTC	ATCATAGTCA	78900
		A			
[exon 4: 78864..					
CGGTGGTGTC	GGTGTGCTG	TCCCTGTTCTG	TGACATCTGT	CCTGCTCTGC	
A					
TTCATCTTCG	GCCAGCACTT	GCGCCAGCAG	CGGATGGGCA	CCTACGGGGT	79000
	A				
GCGAGCGGCT	TGGAGGAGGC	TGCCCCAGGC	CTTCCGGCCA	TAGCAACCAT	
			A		
..79043]					
GAGTGGCATG	GCCACCACCA	CGGTGGTCAC	TGGAACCTCAG	TGTGACTCCT	79100
CAGGGTTGAG	GTCCAGCCCT	GGCTGAAGGA	CTGTGACAGG	CAGCAGAGAC	
TTGGGACATT	GCCTTTTCTA	GCCCGAATAC	AAACACCTGG	ACTTAGCCCT	79200
GTGCCCACAG	TGTCTCCTCC	TGGGATAACA	ATGGCCAGGG	AGGGGAGCCA	
CCATGGGGGA	CCCCTCTCCC	TAGATGCCTC	CCTCCCCACC	CTCTCCTTCA	79300
CAGGGGCCTC	CCAGCCCATG	CAACAGGCCC	CCATCTGGCC	CGAGTAGCTC	
ATTGCTACTG	AGGGAGGGTG	GGGGAAACAC	ACCCTGGCCC	AGGGGGCAGA	79400
GGACACACTG	TTCCCACCTG	GCCCCAGGAG	ACCTCAGGCC	ACTCCTGGCC	
ACAGCAGGAC	AAAGCTCTGA	CCTCTCCTTT	CTGCCAACAG	AGCTGCTTCC	79500
TGGGATGAGG	GGTGGGGGGC	CCAGCGAACT	GACTCTGCTC	AGGGGCGCTG	
CCCAGCAAAG	TCTCTCCCCG	ACCCTCTGG	GCCCCTCCAG	CCACCTCAAA	79600
GGGGCCTTCA	AAGCTGTGGA	AAGCAGAAGG	AATCCCCCCC	TCCCCTCTTG	
CTCCATTACT	AGGCTGGAAG	GAGACCTCAT	CATCCCAGAG	AGAGGGGTGA	79700
GGGAGAGAGG	GTGGGGGCTC	TGTTCACAGG	CCTCCCCCTG	CTCCAGGCAG	
GAAGCAGTGG	GGCAGAGGCG	GGCTGACGTG	GCTTCAAGGG	CCTGGGTGGT	79800
GCTCTAGGGA	GCTCTTACAC	AACAGCACAG	ATCCGGCCCC	TCCAGGAACT	
CATTGGCGTG	GGGCAGGGAC	TGATTTCCCC	AGGAGAAGAG	GGCCTGGCTG	79900
AGGTTGAGGG	AGTGAGAAGG	ACTGCCAGCC	ATGGGCACCG	GGGAGTCGAC	
AAGAGAGGTG	CAGGAGGCGG	CTCCGGGGCT	GTATCCAGAG	CAGGAAGCTG	80000
GTGCAGTTCC	CAGGGCCGGG	GTCTGTCCTC	ATAGGAGGCT	CTCGGCATCA	
TAGTAGTCTG	GGGAAACAAG	AACCTCATCT	TGACTCCCTC	CTGTCTCAGT	80100
GGACCCCAAA	GAGGTAAAGG	GAAGGGGACA	GGCCAGTTGC	CTGCAGCAGT	
GATGTTAGGA	AACCCCAAAA	CCCCACCAGA	GGGCACAGGG	CCCTCCTGGC	80200
CTCCTGATTC	ACTCCCAGGC	CTGGGCCCCG	CTGCCACCA	CCCCAGCCCT	
ACCTGAAGCC	GGGGGTACAT	CAGCACCCAC	AGTCCCTGTG	GCACTGGGGG	80300
GTGGGGGTGG	GGGCACAGCT	CTCCTGAGAT	GGGGGAAAGA	AAAAGACCCC	
CATCAGAGGC	CCAGGGGTGG	CCTCTGGAGT	TTACCCACA	AGTTATCTCC	80400

FIGURE 1D

5/8

ACCGACCACC	AGCCCCTGCA	CAGCTCTTCT	GCAACTTCCA	GCCCAGAGCA	
GAACCCTGGC	AGCACCCAGC	CTCACTTACA	CCTCCCTTTC	CCTGGAGGCA	80500
GGACAGTGCT	GAATCCTGGG	CACGTCCTGC	AAGTAGGGCT	GACAAGCAGG	
GGTGGGGAAG	AAGGGGGCTG	GCCAGGGCAG	CAGGGCACCC	GGGGAGGGCA	80600
TCAAATAGGG	CAAGTAGTGG	TGGTGAAACA	CCAAAGGCCC	TTTCTCCCGC	
ACGTCCATCT	CCTCCTCCTC	CTCCTCAGGC	TCTTCCTGTG	GAACCTCCAG	80700
GTAGACCTGG	GGATTGTGCA	AAACAGGGAG	GGGAAATGAG	AATCTACCAT	
CAGGCTCTCC	CCACCGCCAC	TCCTCCATTC	CCCTAAGTTA	TTTCCTCCAG	80800
ATAGGCTTTG	TAAGAATGGC	TTGTGGCCAG	GCATGGTGGC	TCACGCCTGT	
AATCCCAGCA	CTGTGGGAGG	CCGAGGCGGG	CGGATCACAA	GGTCAGGAGA	80900
TTGAGACCAT	CCTGGCTAAC	ACGGTGAAAC	CCCGTCTCTA	CTAAAAATAC	
CAAAAAAAAA	AAAAAAAAAA	TTAGCTGGGC	ATGGTGGTGG	GCGCCTGTAG	81000
TCCCAGCTAC	TCAGGAGGCT	GAGGCAGGAG	AATGGCGTGA	ACCCGGGAGG	
CGGAGCTTGC	AGTGAGCAGA	GATCGAGCTA	CTGCACTCCA	GCCTGGGCGG	81100
CAGAGCGAGA	CTCCATCTCA	AAAGAAAAAA	AAGGAAAAAA	AAAAAAGAA	
TGGCTTGTGT	AGGCGGGGCG	CGGTGGCTCA	TGCCTGTAAT	CCCGGCACTT	81200
TGGGAGGCTG	AGGCGGACGG	ATCACAAAGGT	CAGGAGATCG	AGACCATCCT	
GGCTAACATA	GTGAAACCCC	GTCTCTACTA	AAAACACAAA	AAAGTAGCCG	81300
GGTGTGGTGG	CAGGCGCCTG	TGGTCCCAGC	TACTCGGGAG	GCTGGGGCAG	
GAGAGTTGTT	TGAACCCAGG	AGGTGGAAGT	TGCAGTGTGC	CGAGATTGCA	81400
TCACTATACT	CCAGCCTAGG	TGACAGAGAG	AGACTCCGTC	TCAAAAAAAA	
GAAAAAGAAA	AGAAAAGAAA	AAAAGAATGG	GTTGTGTTTA	TTGAGCGTTT	81500
ACTACATGCG	GACAACAAAT	TGTGGAGACA	TTTACTCCTG	TAGCTCAAGG	
ACGTTGAGCA	ACTTGGCCAC	CCAGTTGATT	CCAGGTGTGA	CCCCCAGAGC	81600
TGGGGCCAGG	AGTCCACTGA	GCTGTCCCCG	GCCTCACCCC	CGGCCCCTGG	
ACCCACCTAT	GTGTCATCAC	TGAGGACCCA	GGGGTGAGGG	GTGGCAGTAG	81700
CTCCTCAGGG	TCTCCTTCTG	TCTGGATTCC	TTGAACCCCT	CTCCGCCTCC	
TCCGAGCTGA	ACAACATTTCT	CTCTCCACCC	AGTCCCTGCT	TCTCCTGACC	81800
TCAGGATGCC	CACTATTGGC	TGAGTAAGGC	TCAGCCTTAG	AGCTATATGC	
ACATGCATGC	ACACACACGC	TTGCACACAC	CCCCACTTGC	ACACACTTGC	81900
TTGCACGCAC	ACACTTGCTT	GCACGCACAC	ACTTGCCTTC	ACAACCCGCT	
CGCACACACG	TGCACGCACA	CCCTTGACACA	CGCACGTGAA	CACACACTTG	82000
CACACACATA	TGCATGTACA	CAGCCTTGCA	CACACACACG	CATGCACACA	
GACACCCACT	TGCACACACA	TACACACACA	CACTCTTGCA	CACACACACT	82100
GCCGCACACG	GTTTCCCCCA	TTCTGTCTCC	TGACTCTGCC	CCTGCCAGCC	
TGGATGGGGG	ACACACCCTT	CGCCTCCTCC	AAGGGTCAAA	ATCCTACCTG	82200
GCTTTCAAGG	GCTGGTTCTA	AGATCCTCTG	CTCCTCCAAG	GAGCCTGTCC	
CCATCCCCCA	ACCCTATGTG	CACTTGTGCT	TTGTACCTCT	CCATGTGCCA	82300
TCACAGCCAA	CCTGGCTTTG	TATCCCTAAC	CATTCATTTA	TTCATTCACT	
CGTTCAACAA	ATATCAGCTG	AGCCCCTACA	CGGTGTCAGG	CACCAGGCCA	82400
GACGCTCATG	ATGCATGGGG	CAGGGTTACC	AGGGTGCCTA	CCTTCCTGGA	
GCCTTAAGTC	CAGTGGGGGA	GGCACTACAG	GGAAACCTCC	TTGAAAACAA	82500
GACCTCGGTG	GTCTGGACTT	TGGGGGGTCT	CTTCCCCGCC	CCAACCTTTC	
ATGGAGGCTG	AAACATGACA	GATGCCAAAC	AGCCCCAGCC	AGAGAGACGG	82600
GCTGGCTTCC	TGCTCCTCTG	TCTCCCAGTT	CTTTTCCCCC	CTGAACAGGA	
ACCCAGGTG	GATCCGCATC	CCTGGACCCA	CAGGTGAGCG	ACCCCGGCGG	82700
CCCACCCACA	CGCACCTGAG	GGCAGGGCGA	GGCAGGCCGG	GGCTGCAGCG	
CTCCAGCCAC	CAGGCGACTC	AGCAGCAGCT	GGTGCATCTG	CGCGTTCTGC	82800
AGCATCATCA	GTTCCAGCAG	GTCTAGGAAG	CGGGGTTCAG	CAAGCCCACG	
CCGGGCCTCC	GAGTCCCCCT	CCCCCTGACA	CCCCTGTCCC	GGGGGTGAAG	82900
AATGGGTGTTG	CGGGTTGTGC	TGCGGGGACT	CCCAGAGGAT	GTGCGAGGCA	
GAAGAGGGTG	AGTGGTGGTG	ATGGTGGGGG	TGGGGTGGGG	GGACCCGGGA	83000

FIGURE 1E

[illegible]

2

GTCTCACCTT CCTTCACGCG GCCTGGCTGC GGGGGCGCAG GTG

83043

FIGURE 1F

7/8

POLYMORPHISMS IN THE CODING SEQUENCE OF ICAM2

ATGTCCTCTT	TCGGTTACAG	GACCCTGACT	GTGGCCCTCT	TCACCCTGAT	
	T			G	
CTGCTGTCCA	GGATCGGATG	AGAAGGTATT	CGAGGTACAC	GTGAGGCCAA	100
AGAAGCTGGC	GGTTGAGCCC	AAAGGGTCCC	TCGAGGTCAA	CTGCAGCACC	
ACCTGTAACC	AGCCTGAAGT	GGGTGGTCTG	GAGACCTCTC	TAGATAAGAT	200
TCTGCTGGAC	GAACAGGCTC	AGTGGAAACA	TTACTTGGTC	TCAAACATCT	
CCCATGACAC	GGTCCTCCAA	TGCCACTTCA	CCTGCTCCGG	GAAGCAGGAG	300
TCAATGAATT	CCAACGTCAG	CGTGTACCAG	CCTCCAAGGC	AGGTCATCCT	
GACACTGCAA	CCCAC TTTGG	TGGCTGTGGG	CAAGTCCTTC	ACCATTGAGT	400
GCAGGGTGCC	CACCGTGGAG	CCCCTGGACA	GCCTCACCCCT	CTTCCTGTTC	
CGTGGCAATG	AGACTCTGCA	CTATGAGACC	TCGGGAAGG	CAGCCCCTGC	500
TCCGCAGGAG	GCCACAGCCA	CATTCAACAG	CACGGCTGAC	AGAGAGGATG	
GCCACCGCAA	CTTCTCCTGC	CTGGCTGTGC	TGGACTTGAT	GTCTCGCGGT	600
GGCAACATCT	TTCACAAACA	CTCAGCCCCG	AAGATGTTGG	AGATCTATGA	
GCCTGTGTCG	GACAGCCAGA	TGGTCATCAT	AGTCACGGTG	GTGTCGGTGT	700
	A		A		
TGCTGTCCCT	GTTCGTGACA	TCTGTCCTGC	TCTGCTTCAT	CTTCGGCCAG	
				A	
CACTTGCGCC	AGCAGCGGAT	GGGCACCTAC	GGGGTGCGAG	CGGCTTGGAG	800
GAGGCTGCCC	CAGGCCTTCC	GGCCATAG			828
		A			

FIGURE 2

8/8

ISOFORMS OF THE ICAM2 PROTEIN

MSSF	GYRTL	T	VAL	FTLIC	CP	GSDE	KVFE	VH	VRPK	KLAVE	P	KGS	LEV	NC	ST	
A																
TCNQ	PEVG	GL	ETSL	DKILL	D	EQAQ	WKHY	LV	SNIS	HDTV	LQ	CHFT	CSG	KQE		100
SMNS	NVSV	YQ	PPRO	VILT	LQ	PTLV	AVGK	SF	TIEC	RVPT	VE	PLDS	LTFL	FLF		
RGNE	TLHY	ET	FGKA	APAP	QE	ATAT	FNST	AD	REDG	HRNF	SC	LAVL	DLMS	RG		200
GNIF	HKHS	AP	KMLE	IYEP	VS	DSQM	VIIIV	TV	VSVL	LSLF	VT	SVLL	CFIF	FGQ		
D																
HLRQ	QRMG	TY	GVRA	AWRR	LP	QA	FR	P								275

FIGURE 3